AMENDMENT

Please amend the above-captioned application as follows:

In The Claims:

Please cancel claims 1, 15, 21, 23 to 43, without prejudice.

Please amend the claims to read as follows:

--2. (Amended) The computer program product of claim 53, wherein the subset of amino acid residues comprising the amino acid identity constraint of step (a) comprises 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acid residues or sets of amino acid residues.

3. (Amended) The computer program product of claim 53, wherein the identity of an amino acid residue specified in the functional site descriptor is selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

4. (Amended) The computer program product of claim 53, wherein the identity of an amino acid residue specified in the functional site descriptor comprises a set of two or more amino acid residue identities, wherein each of said amino acid residue identities is selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

5. (Amended) The computer program product of claim 53, wherein each geometric constraint within the set of geometric constraints is selected from the group consisting of an atomic position specified by a set of three dimensional coordinates, an interatomic distance, and an interatomic bond angle.

6. (Twice amended) The computer program product of claim 5, wherein at least one member of the set of geometric constraints is an atomic position specified by a set of three dimensional coordinates, wherein the atomic position can vary within a preselected root mean square deviation.

7. (Twice amended) The computer program product of claim 6, wherein the atomic position varies within a root mean square deviation of less than about 3 Å.

8. (Amended) The computer program product of claim 5, wherein at least one member of the set of geometric constraints is an interatomic distance.

9. (Amended) The computer program product of claim 5, wherein at least one member of the set of geometric constraints is an interatomic bond angle range.

10. (Amended) The computer program product of claim 53, further comprising a conformational constraint.

11. (Amended) The computer program product of claim 53, wherein the one or more geometric constraints of step (b) comprises at least one atom from each of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acid residues that comprise the functional site.

12. (Amended) The computer program product of claim 53, wherein all of the atoms for which geometric constraints are provided comprise a part of the protein backbone and are selected from the group consisting of an α-carbon, an amide nitrogen, a carbonyl carbon and a carbonyl oxygen.

13. (Amended) The computer program product of claim 53, wherein at least one of said one or more atoms is a pseudoatom.

14. (Amended) The computer program product of claim 13, wherein the pseudoatom is a center of mass with respect to at least two atoms selected from the group consisting of an atom from one amino acid residue and an atom from at least two amino acid residues of the protein.

16. (Amended) The computer program product of claim 53, wherein the functional site descriptor defines a functional site of a protein comprising biological function selected from the group consisting of a disulfide oxidoreductase activity, a α/β hydrolase activity, a phospholipase activity, and a T1 ribonuclease activity.

17. (Amended) The computer program product of claim 53, wherein the functional site descriptor is selected from the group consisting of a three atom functional site descriptor, a four atom functional site descriptor, a five atom functional site descriptor, a six atom functional site descriptor, a seven atom functional site descriptor, an eight atom functional site descriptor, a nine atom functional site descriptor, a ten atom functional site descriptor, an eleven atom functional site descriptor, a twelve atom functional site descriptor, a thirteen atom functional site descriptor, a fourteen atom functional site descriptor, and a fifteen atom functional site descriptor.

18. (Amended) The computer program product of claim 53, wherein the functional site descriptor is selected from the group consisting of an active site of an enzyme, a ligand binding domain, and a protein-protein interaction domain.

19. (Amended) The computer program product of claim 18, wherein ligand binding domain binds a ligand selected from the group consisting of a substrate, a co-factor, and an antigen.

20. (Amended) The computer program product of claim 53, wherein the computer program product encodes a library of functional site descriptors.

22. (Amended) The computer program product of claim 20, wherein the library comprises at least two functional site descriptors for at least one of the biological functions represented by the library.

44. (Amended) The method of claim 54, wherein the functional site descriptor is selected from the group consisting of an active site of an enzyme, a ligand binding domain, and a protein-protein interaction site.

45. (Amended) A computer program product comprising a computer useable medium having computer program logic recorded thereon for creating a functional site descriptor for use in predicting a biological function of a protein, said computer program logic comprising computer program code logic configured to perform the operations of:

(a) determining a set of geometric constraints for a functional site associated with a biological function of a protein, wherein a set of geometric constraints comprises one or more geometric constraints between at least three different atoms, wherein each atom is in a different amino acid residue of the protein and the different atoms comprise:

(i) an atom of a first amino acid residue of the functional site comprising the amino acid residue of part (a), wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon;

(ii) an atom of a second amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon; and,

(iii) an atom of a third amino acid residue of the protein, wherein the atom is selected from the group consisting of a backbone atom, a side chain atom and a pseudoatom,

(b) modifying one or more geometric constraints of said set of geometric constraints to produce a modified set of geometric constraints,

(c) comparing said modified set of geometric constraints to a data set of functional sites correlated with said biological function to determine whether said modified set of geometric constraints compares positively with said data set of functional sites correlated with said biological function and, if there is a positive correlation:

(d) repeating said modifying and comparing operations of steps b and c to modify one or more of said geometric constraints of said set of geometric constraints to an extent that said modified set of geometric constraints compares positively with said data set of functional sites correlated with said biological function without encompassing a predetermined amount of data sets not correlated with said biological function.

46. (Amended) The computer program product of claim 45, wherein said operation of determining a set of geometric constraints of a functional site correlated with a biological function of a protein comprises receiving said set of geometric constraints from at least one group of a data set of predetermined geometric constraints or from a user input.

47. (Amended) The computer program product of claim 45, wherein said set of geometric constraints concerns one or more atoms in each of two or more amino acid residues comprising a functional site of a protein, wherein at least one of said two or more amino acid residues is identified as a particular amino acid residue or set of amino acid residues,

wherein said one or more atoms is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, beta-carbons of amino acid residues, and pseudoatoms.

48. (Amended) The computer program product of claim 45, wherein said set of geometric constraints further comprises one or more geometric constraints with respect to one or more atoms or pseudoatoms of one or more amino acid residues that are adjacent to an amino acid residue of said two or more amino acid residues.

49. (Amended) The computer program product of claim 45, wherein said set of geometric constraints comprises geometric constraints selected from the group consisting of atomic positions specified by sets of three dimensional coordinates, interatomic distances, and interatomic bond angles.

50. (Amended) The computer program product of claim 45, wherein at least one of the geometric constraints of said set of geometric constraints comprises interatomic distances between one or more atoms and/or pseudoatoms of the amino acid residues of the functional site descriptor.

51. (Amended) The computer program product of claim 45, wherein said operation of modifying one or more geometric constraints of said set of geometric constraints to produce a modified set of geometric constraints comprises associating a predetermined variance with one or more of the geometric constraints.

52. (Amended) The computer program product of claim 45, wherein said operation of modifying one or more geometric constraints of said set of geometric constraints to produce a modified set of geometric constraints comprises:

computing an average value for a geometric constraint within the set of geometric constraints by determining values for said geometric constraint from two different proteins having functional sites that correlate with said biological function, and calculating said average value;

computing a standard deviation with respect to such geometric constraint; and

applying a multiplier to said computed standard deviation to generate said modified geometric constraint.--

Please add the following new claims:

--53. A computer program product encoding a functional site descriptor, wherein the functional site descriptor defines at least one functional site of a protein, other than a divalent metal ion binding site, the functional site descriptor comprising:

(a) an amino acid residue identity constraint for a first amino acid residue of the functional site, wherein the first amino acid residue is identified as a single amino residue or as a subset of amino acid residues; and,

(b) one or more geometric constraints between at least three different atoms, wherein each atom is in a different amino acid residue of the protein and the different atoms comprise:

(i) an atom of the first amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon;

(ii) an atom of a second amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon; and,

(iii) an atom of a third amino acid residue of the protein, wherein the atom is selected from the group consisting of a backbone atom, a side chain atom and a pseudoatom.

54. A computer implemented method for determining a functional site descriptor that defines a spatial configuration of a functional site, wherein the functional site descriptor defines a functional site of a protein other than a divalent metal ion binding site, the method comprising the following steps:

(a) identifying an amino acid residue identity constraint for a first amino acid residue of the functional site, wherein the first amino acid residue is identified as a single amino residue or as a subset of amino acid residues; and,

(b) identifying one or more geometric constraints between at least three different atoms, wherein each atom is in a different amino acid residue of the protein and the different atoms comprise:

(i) an atom of the first amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon;

(ii) an atom of a second amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a

backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon; and,

(iii) an atom of a third amino acid residue of the protein, wherein the atom is selected from the group consisting of a backbone atom, a side chain atom and a pseudoatom, thereby determining a functional site descriptor.

55. The method of claim 54, wherein the spatial configuration of the protein functional site corresponds to at least one biological function.

56. A computer-implemented method for defining a functional site descriptor of a protein comprising the following steps:

(a) identifying an amino acid residue identity constraint for a first amino acid residue of the functional site, wherein the first amino acid residue is identified as a single amino residue or as a subset of amino acid residues; and,

(b) identifying one or more geometric constraints between at least three different atoms, wherein each atom is in a different amino acid residue of the protein and the different atoms comprise:

(i) an atom of the first amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon;

(ii) an atom of a second amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon; and,

(iii) an atom of a third amino acid residue of the protein, wherein the atom is selected from the group consisting of a backbone atom, a side chain atom and a pseudoatom, thereby determining a functional site descriptor.

57. A computer program product for defining a functional site descriptor of a protein comprising a computer useable medium comprising a computer readable program code embodied therein, wherein the computer program product is capable of defining a functional site descriptor of a protein by a process comprising the following steps:

(a) identifying an amino acid residue identity constraint for a first amino acid residue of the functional site, wherein the first amino acid residue is identified as a single amino residue or as a subset of amino acid residues; and,

(b) identifying one or more geometric constraints between at least three different atoms, wherein each atom is in a different amino acid residue of the protein and the different atoms comprise:

(i) an atom of the first amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon;

(ii) an atom of a second amino acid residue of the functional site, wherein the atom is selected from the group consisting of a backbone amide nitrogen, an alpha-carbon, a backbone carbonyl carbon, a backbone carbonyl oxygen, a backbone pseudoatom and a beta-carbon; and,

(iii) an atom of a third amino acid residue of the protein, wherein the atom is selected from the group consisting of a backbone atom, a side chain atom and a pseudoatom, thereby determining a functional site descriptor.

58. A computer system, comprising:

(a) a processor; and

(b) a computer program product as set forth in claim 45.

59. A computer system, comprising:

(a) a processor; and

a computer program product as set forth in claim 53.

60. A computer system, comprising:

(a) a processor; and

a computer program product as set forth in claim 57.--